

## CRF Errors Corrected by the STIC Systems Branch

0420

O1PE #8

7/25/2002

Serial Number: 097887,540A

CRF Processing Date:

Edited by:

Verified by: A (STIC sta

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:  
\_\_\_\_\_

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_.

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:  
\_\_\_\_\_

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  
\_\_\_\_\_

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  
\_\_\_\_\_

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:  
\_\_\_\_\_

Deleted extra, invalid, headings used by an applicant, specifically:  
\_\_\_\_\_

Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  page numbers throughout text;  other invalid text, such as \_\_\_\_\_

Inserted mandatory headings, specifically: \_\_\_\_\_

Corrected an obvious error in the response, specifically: \_\_\_\_\_

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

Other:  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/887,540A

DATE: 07/25/2002  
TIME: 16:07:57

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF3\07252002\I887540A.raw

4 <110> APPLICANT: Klein, Robert  
 6 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING LPR5 GENE  
 7       DISRUPTIONS  
 9 <130> FILE REFERENCE: R-193  
 11 <140> CURRENT APPLICATION NUMBER: US 09/887,540A  
 12 <141> CURRENT FILING DATE: 2001-06-21  
 14 <150> PRIOR APPLICATION NUMBER: US 60/213,201  
 15 <151> PRIOR FILING DATE: 2000-06-21  
 17 <150> PRIOR APPLICATION NUMBER: US 60/223,123  
 18 <151> PRIOR FILING DATE: 2000-08-07  
 20 <160> NUMBER OF SEQ ID NOS: 4  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 5119  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Mus musculus  
 29 <400> SEQUENCE: 1  
 30 gccggggcgc ccgaggcggg agcaagaggc gcccggagcc gcgaggatcc accggccgccc 60  
 31 cgcgcgcccgt ggagcccgag tgagcgcgcg ggcgtccccc cccgcggacg acatggaaac 120  
 32 ggcgcgcacc cgggcgcctc cggcgcgcgc gccgcgcgtg ctgtctgtgg tgctgtactg 180  
 33 cagcttggtc cccgcgcgcg cctcaccgcgt cctgtgttt gccaaccgcc gggatgtgcg 240  
 34 gctagtggat gcccggag tgaagctgga gtccaccatt gtggccagtgc gcctggagga 300  
 35 tgcagctgtgt gtagacttcc agttctccaa gggtgctgtg tactggacag atgtgagcga 360  
 36 ggaggccatc aaacagacact acctgaacca gactggagct gctgcacaga acatgtcat 420  
 37 ctcgggcctc gtgtcacctg atggcctggc ctgtactgg gttggcaaga agctgtactg 480  
 38 gacggactcc gagaccaacc gcattgaggt tgccaaacctc aatgggacgt cccgttaagg 540  
 39 tctcttctgg caggacctgg accagccaag ggcattgcc ctggatccctg cacatggta 600  
 40 catgtactgg actgactggg gggaaagcacc cccgatcgag cgggcaggga tggatggcag 660  
 41 taccggaaat atcattgttag actccgacat ttactggccc aatgggctga ccattcgacct 720  
 42 ggaggaacag aagctgtact gggccatgc caagctcagc ttcatccacc gtgccaacct 780  
 43 ggacggctcc ttccggcaga aggtggtgg gggcgcgcctc actcaccctt ttgcctgac 840  
 44 actctctgg gacacactct actggacaga ctggcagacc cgctccatcc acgcctgcaa 900  
 45 caagtggaca ggggagcaga ggaaggagat ctttagtgct ctgtactcac ccattggacat 960  
 46 ccaagtgtgt agccaggagc ggcagccccc cttccacaca ccattgcgagg aggacaacgg 1020  
 47 tgctgttcc cacctgtgcc tgctgtcccc gagggagcct ttctactctt gtgcctgccc 1080  
 48 cactgggtgt cagttgcagg acaatggcaa gacgtgcaag acaggggctg aggaagtgt 1140  
 49 gctgctggct cggaggacag acctgaggag gatctctgt gacacccctg acttcacaga 1200  
 50 catagtgtgt cagggtggcg acatccggca tgccattgcc attgactacg atcccctgga 1260  
 51 gggctacgt tactggaccc atgatgaggt gcccgtatc cgcaggccgt acctagatgg 1320  
 52 ctcaggtgcg cagacacttg tgaacactga gatcaatgac cccgatggca ttgtgtgg 1380  
 53 ctgggtcgcc cggaaacctct actggacaga tacaggcact gacagaattg aggtgactcg 1440  
 54 cctcaacggc acctcccgaa agatcctgtt atctgaggac ctggacgaac cgcgagccat 1500  
 55 tttgtttgcac cctgtatgg gcctcatgtt ctggacagac tggggggaga accccaaaat 1560

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56 cgaatgcgcc aacctagatg ggagagatcg gcatgtcctg gtgaacacct cccttgggt 1620  
57 gcccaatgga ctggccctgg acctgcagga gggcaagctg tactgggggg atgc当地 1680  
58 tgataaaaatc gaggtgatca acatagacgg gacaaagcgg aagaccctgc ttgaggacaa 1740  
59 gctcccacac attttgggt tcacactgct gggggacttc atctactgga ccgactggca 1800  
60 gagacgcagt attgaaaggg tccacaaggc caaggccagc cgggatgtca tcattgatca 1860  
61 actccccgac ctgatgggac tcaaagccgt gaatgtggcc aagggtgtcg gaaccaaccc 1920  
62 atgtgcggat ggaaatggag ggtgcagcca tctgtcttc ttccacccac gtgc当地 1980  
63 gtgtggctgc cccattggcc tggagctgtt gagtgacatg aagacctgca taatccccga 2040  
64 ggccttcctg gtattcacca gcagagccac catccacagg atctccctgg agactaacaa 2100  
65 caacgatgtg gctatccac tcacgggtgt caaagaggcc tctgcactgg actttgatgt 2160  
66 gtccaacaat cacatctact ggactgtatg tagcctcaag acgatcagcc ggc当地 2220  
67 gaatggagc tcagtggagc acgtgattga gtttggcctc gactaccctg aaggaatggc 2280  
68 tgtggactgg atgggcaaga acctctattg ggc当地 gggacaca ggaccaaca ggattgaggt 2340  
69 ggccggctg gatgggcagt tccggcagggt gcttgggtgg agagaccttg acaacccag 2400  
70 gtctctggct ctggatctta ctaaaggctt catctactgg actgagtggg gtggcaagcc 2460  
71 aaggattgtg cgggccttca tggatgggac caattgtatg acactggtag acaaggtggg 2520  
72 cccggccaaac gacccatcca ttgattatgc cgaccagcga ctgtactgga ctgacccctg 2580  
73 caccaacatg attgagttt ccaacatgct ggttcaggag cgc当地 tagctgacga 2640  
74 tctgccttac cgggttggcc tgactcaata tagcgattac atctactgga ctgactggaa 2700  
75 cctgcatacg attgaacggg cggacaagac cagtgccgg aaccgcaccc tc当地 2760  
76 tcacctggac ttctgtcatgg acatctgggt gttccactcc tcccgtcagg atggcctcaa 2820  
77 cgactgcgtg cacagcaatg gccagttgtgg gcagctgtgc ctgc当地 cc当地 2880  
78 ccgctgtggc tggcttcac actacacgct ggacccagc agccgcaact gc当地 2940  
79 ctccacccctt tggctttca gccagaaatt tgccatcagc cggatgatcc cc当地 3000  
80 gctcagcccg gaccccttcc tacccttca tgggctgagg aacgtcaaaag ccatcaacta 3060  
81 tgaccccgatg gacaaggcttca tctactgggt ggacggccgc cagaacatca agagggccaa 3120  
82 ggacgcacggt accccaggccct ccatgtgtac ctctccagc caaagccctgaa gccc当地 3180  
83 acagccacac gacccatcca ttgacccatcta cagccggaca ctgttctgga cctgtgaggc 3240  
84 caccaacact atcaatgtcc accggctggaa tgggatgccc atgggatgtgg tgctcgagg 3300  
85 ggaccgtgac aagccaaaggg ccattgtgtt caatgtgtgg cgagggtaca tgc当地 3360  
86 caacatgcag gaccatgtt ccaagatcga gcgacccctt cc当地 cc当地 3420  
87 ggtcccttcc accacaggcc tcatccgtcc cgtggccctt gtggatggaca atgc当地 3480  
88 caagcttcc tgggtggatg cc当地 ccatcttgc gcaatcga agctgtgacc tctctggg 3540  
89 caaccgcctg acccttggaaatg ctttccatc cgtacagcca gtaggtctgaa cagtgctggg 3600  
90 caggcacccct tactggatcg accggccagca gc当地 gacccctt cc当地 3660  
91 tggggacaag cggacttaggg ttccaggccct tgc当地 cttccatc cttccatc 3720  
92 ggaggaagtc agcctggagg agtttccatc cc当地 ccatcttgc gccgagaca atggccgtg 3780  
93 ctcccacatc tggatcgttcc agggatgtgg aacaccggcc tgctcgttcc ctgatc 3840  
94 ggtgctctg cagaacccatc tgacttgc tggatgtgg tgatcgttcc ctgatc 3900  
95 tgc当地 tggatgttcc actggatgttcc tggatgttcc cccggagcc tggatgttcc acggcc 3960  
96 tggatgttcc gaccaggatg atggatgttcc cttccatc cttccatc cttccatc 4020  
97 ctgc当地 tggatgttcc tggatgttcc gttacccatc gacccatc gtaggttcc 4080  
98 ggatcgttcc gatggatgttcc actggatgttcc tggatgttcc cccatc gtaggttcc 4140  
99 cagcggccag tggatgttcc tggatgttcc tggatgttcc tggatgttcc 4200  
100 gtc当地 tggatgttcc cttccatc cttccatc cttccatc cttccatc 4260  
101 cttccatc cttccatc cttccatc cttccatc cttccatc cttccatc 4320  
102 cttccatc cttccatc cttccatc cttccatc cttccatc cttccatc 4380  
103 cttccatc cttccatc cttccatc cttccatc cttccatc cttccatc 4440  
104 cttccatc cttccatc cttccatc cttccatc cttccatc cttccatc 4500

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105 gggggggcgc ggcagcgtgc ccctctatga ccggaatcac gtcactgggg cctcatccag 4560  
 106 cagctcgtdcc agcacaaagg ccacactata tccggcgatc ctgaaccac ccccggtcccc 4620  
 107 ggccacagac ccctctctt acaacgtgga cgtttttat tcttcaggca tcccgccac 4680  
 108 cgcttagacca tacaggccct acgtcattcg aggtatggca cccccaaca caccgtgcag 4740  
 109 cacagatgtg tgtgacagtg actacagcat cagtcgtgg aagagcagca aatactacct 4800  
 110 ggacttgaat tcggactcag acccctaccc ccccccggcc acccccccaca gccagttac 4860  
 111 atctgcagag gacagctgcc caccctcacc aggeactgag aggagttact gccaccttt 4920  
 112 cccgccccca ccgtccccct gcacggactc gtcctgaccc cggccgtcca cccggccctg 4980  
 113 ctgcctccct gtaaatattt ttaaatatga acaaaggaaa aatatatttt atgatttaaa 5040  
 114 aaataaaat aattggggtt ttaacaagt gagaatgtg agcggtaag gggtgggcag 5100  
 115 ggctgggaaa cttttctag 5119  
 117 <210> SEQ ID NO: 2  
 118 <211> LENGTH: 1614  
 119 <212> TYPE: PRT  
 120 <213> ORGANISM: Mus musculus  
 122 <400> SEQUENCE: 2  
 123 Met Glu Thr Ala Pro Thr Arg Ala Pro Pro Pro Pro Pro Pro Pro Pro Leu  
 124 1 5 10 15  
 125 Leu Leu Leu Val Leu Tyr Cys Ser Leu Val Pro Ala Ala Ala Ser Pro  
 126 20 25 30  
 127 Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala Gly  
 128 35 40 45  
 129 Gly Val Lys Leu Glu Ser Thr Ile Val Ala Ser Gly Leu Glu Asp Ala  
 130 50 55 60  
 131 Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr Asp  
 132 65 70 75 80  
 133 Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly Ala  
 134 85 90 95  
 135 Ala Ala Gln Asn Ile Val Ile Ser Gly Leu Val Ser Pro Asp Gly Leu  
 136 100 105 110  
 137 Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu Thr  
 138 115 120 125  
 139 Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val Leu  
 140 130 135 140  
 141 Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala Leu Asp Pro Ala  
 142 145 150 155 160  
 143 His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Ala Pro Arg Ile Glu  
 144 165 170 175  
 145 Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser Asp  
 146 180 185 190  
 147 Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys Leu  
 148 195 200 205  
 149 Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu Asp  
 150 210 215 220  
 151 Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro Phe  
 152 225 230 235 240  
 153 Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln Thr  
 154 245 250 255  
 155 Arg Ser Ile His Ala Cys Asn Lys Trp Thr Gly Glu Gln Arg Lys Glu

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156	260	265	270	
157	Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser Gln			
158	275	280	285	
159	Glu Arg Gln Pro Pro Phe His Thr Pro Cys Glu Glu Asp Asn Gly Gly			
160	290	295	300	
161	Cys Ser His Leu Cys Leu Leu Ser Pro Arg Glu Pro Phe Tyr Ser Cys			
162	305	310	315	320
163	Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly Lys Thr Cys Lys			
164	325	330	335	
165	Thr Gly Ala Glu Glu Val Leu Leu Ala Arg Arg Thr Asp Leu Arg			
166	340	345	350	
167	Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln Val			
168	355	360	365	
169	Gly Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu Gly			
170	370	375	380	
171	Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala Tyr			
172	385	390	395	400
173	Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn Asp			
174	405	410	415	
175	Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp Thr			
176	420	425	430	
177	Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr Ser			
178	435	440	445	
179	Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile Val			
180	450	455	460	
181	Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu Asn			
182	465	470	475	480
183	Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Arg Asp Arg His Val Leu			
184	485	490	495	
185	Val Asn Thr Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu Gln			
186	500	505	510	
187	Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu Val			
188	515	520	525	
189	Ile Asn Ile Asp Gly Thr Lys Arg Lys Thr Leu Leu Glu Asp Lys Leu			
190	530	535	540	
191	Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp Thr			
192	545	550	555	560
193	Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala Ser			
194	565	570	575	
195	Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys Ala			
196	580	585	590	
197	Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Gly Asn			
198	595	600	605	
199	Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro Arg Ala Thr Lys Cys			
200	610	615	620	
201	Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys Ile			
202	625	630	635	640
203	Ile Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Thr Ile His Arg			
204	645	650	655	

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205 Ile Ser Leu Glu Thr Asn Asn Asp Val Ala Ile Pro Leu Thr Gly  
 206 660 665 670  
 207 Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His Ile  
 208 675 680 685  
 209 Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg Ala Phe Met Asn  
 210 690 695 700  
 211 Gly Ser Ser Val Glu His Val Ile Glu Phe Gly Leu Asp Tyr Pro Glu  
 212 705 710 715 720  
 213 Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp Thr  
 214 725 730 735  
 215 Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg Gln  
 216 740 745 750  
 217 Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu Asp  
 218 755 760 765  
 219 Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro Arg  
 220 770 775 780  
 221 Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val Asp  
 222 785 790 795 800  
 223 Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln Arg  
 224 805 810 815  
 225 Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn Met  
 226 820 825 830  
 227 Leu Gly Gln Glu Arg Met Val Ile Ala Asp Asp Leu Pro Tyr Pro Phe  
 228 835 840 845  
 229 Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn Leu  
 230 850 855 860  
 231 His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr Leu  
 232 865 870 875 880  
 233 Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His Ser  
 234 885 890 895  
 235 Ser Arg Gln Asp Gly Leu Asn Asp Cys Val His Ser Asn Gly Gln Cys  
 236 900 905 910  
 237 Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys Ala  
 238 915 920 925  
 239 Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro Ser  
 240 930 935 940  
 241 Thr Phe Leu Leu Phe Ser Gln Lys Phe Ala Ile Ser Arg Met Ile Pro  
 242 945 950 955 960  
 243 Asp Asp Gln Leu Ser Pro Asp Leu Val Leu Pro Leu His Gly Leu Arg  
 244 965 970 975  
 245 Asn Val Lys Ala Ile Asn Tyr Asp Pro Leu Asp Lys Phe Ile Tyr Trp  
 246 980 985 990  
 247 Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr Gln  
 248 995 1000 1005  
 249 Pro Ser Met Leu Thr Ser Pro Ser Gln Ser Leu Ser Pro Asp Arg Gln  
 250 1010 1015 1020  
 251 Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp Thr  
 252 1025 1030 1035 1040  
 253 Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu Asp Gly Asp Ala

**VERIFICATION SUMMARY**

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